

Characterization of the complete mitochondrial genome of the common smoothhound shark, *Mustelus mustelus* (Carcharhiniformes: Triakidae)

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ABSTRACT

We present the complete mitochondrial genome of the common smoothhound, *Mustelus mustelus*, which is 16,755 bp long, contains 13 protein-coding genes, 22 tRNA genes, 2 rRNA genes, and non-coding control region. All protein-coding genes begin with the ATG codon, except for the *COI* gene, which begins with GTG. Six protein-coding genes terminated with the TAA codon, and six with incomplete codons, T or TA. The phylogenetic reconstruction places *M. mustelus* within the genus *Mustelus*, with the closest relationship to the placental species, *M. griseus*. This mitogenome provides valuable information to further unravel the evolution of alternate reproductive modes within the genus.

ARTICLE HISTORY

Received 5 July 2018
Accepted 29 July 2018

KEYWORDS

Carcharhiniformes; smoothhound; mitogenome; *Mustelus mustelus*; phylogenetic analysis



The common smoothhound, *Mustelus mustelus* (Linnaeus 1758), is a medium-sized epibenthic shark, distributed from the Mediterranean and eastern Atlantic to the south-west Indian Ocean (Weigmann 2016), with the reproduction mode being placental viviparity (Saidi et al. 2008).

In this study, a specimen was collected by the Department of Agriculture, Forestry and Fisheries, South Africa during tagging surveys off the south-west coast of South Africa (Langebaan Lagoon, Western Cape, latitude: 33°06' S, longitude: 18°01' E). Total genomic DNA was extracted (Elasmobranch Genetics, Lab 242, SU) from a fin clip sample (LL5MM) using a cetyltrimethylammonium bromide extraction protocol of Sambrook and Russell (2001) and sent to the Agricultural Research Council Biotechnology Platform, South Africa for high throughput sequencing. One microgram of genomic DNA was used for 2 × 250 bp paired-end library preparation with a mean insert size of 400 bp using the Illumina TruSeq[®] DNA library preparation kit (Illumina). The library was sequenced on two lanes of an Illumina HiSeq[™] 2000 sequencer.

The generated reads were submitted to quality control as per Maduna et al. (2017). Mitochondrial sequences were filtered from the data set by conducting a BLASTn search (maximum E-value 1.0 E−20) against the mitogenome of *M. griseus* (Genbank accession NC_023527.1, Chen et al. 2016) in Geneious v10.1 (Kearse et al. 2012). These putative mitochondrial sequences were mapped against the mitogenome of *M. griseus* using the Geneious Read Mapper algorithm, with default parameters. The mitogenome was then annotated using the MitoFish and MitoAnnotator web service (Iwasaki et al. 2013).

To infer the phylogenetic placement of *M. mustelus*, the mitogenome of the species (Genbank Accession MH559351) was aligned against 31 complete mitogenomes representing the eight orders of sharks (Figure 1) using MAFFT (Katoh and Standley 2013), with default parameters. The nucleotide substitution model that best fit the alignment was determined in JMODELTEST v2.0 (Darriba et al. 2012) according to the Bayesian Information Criterion, with the GTR+I+G model being the best fit. Bayesian inference of the phylogenetic relationships among mitogenomes was performed in MRBAYES v3.2.6 (Ronquist et al. 2012) with 2,000,000 MCMC generations and the first 500,000 generations discarded as burn-in, performed through the CIPRES Science Gateway (Miller et al. 2010). The consensus tree (Figure 1) was visualized in FIGTREE v1.4.3 (<http://tree.bio.ed.ac.uk/software/figtree>).

The assembled mitogenome of *M. mustelus* is 16,755 bases in length and displayed synteny with other shark and broader vertebrate mitogenomes. The overall base composition of the genome was: A: 31%, T: 30%, C: 25%, and G: 14%. The phylogenetic reconstruction shows the phylogenetic placement of *M. mustelus* within the genus *Mustelus* with the closest relationship to the placental species, *M. griseus*. The positioning of the species could be explained by reproductive mode, as *M. mustelus* and *M. griseus* are viviparous placental, in contrast to *M. manazo*, which is aplacental (Teshima and Koga 1973; Smale and Compagno 1997). Therefore, the mitogenome for *M. mustelus* is an important resource for future conservation and evolutionary biology research such as in-depth phylogenetic placement of species of *Mustelus* with alternate modes of reproduction.

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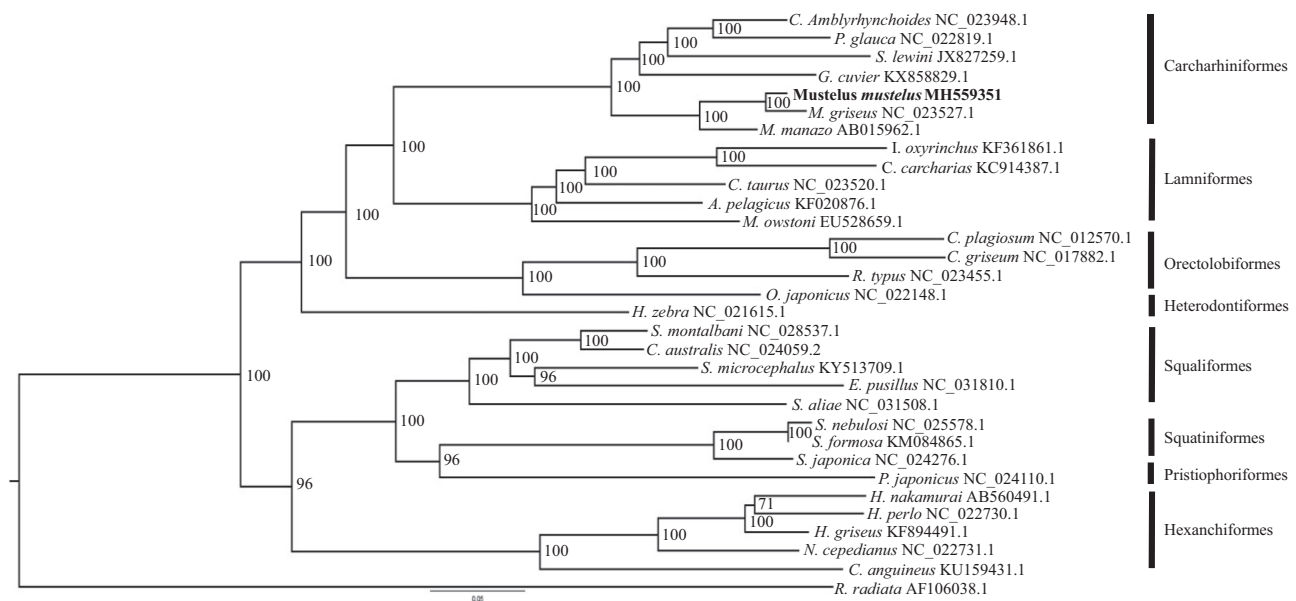


Figure 1. Phylogenetic relationships between the eight orders of shark constructed using Bayesian inference from 31 whole mitogenome sequences, with the thorny skate (*Raja radiata*) mitogenome included as an outgroup. Numbers at nodes indicate posterior probabilities. Genbank accession numbers are given adjacent to the species name, and scale bar indicates groupings of species into orders.

Acknowledgments

This research did not receive any specific grant but was partly funded by the National Research Foundation of South Africa. The authors would like to acknowledge the field work of the Department of Agriculture, Forestry and Fisheries, South Africa for the provision and identification of the sample utilized in the present study.

Disclosure statement

The authors declare no conflict of interest and were solely responsible for the content and writing of this paper.

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References

- Chen X, Peng Z, Pan L, Shi X, Cai L. 2016. Mitochondrial genome of the spotless smooth-hound *Mustelus griseus* (Carcharhiniformes: Triakidae). *Mitochondrial DNA A DNA Mapp Seq Anal.* 27:78–79.
- Darriba D, Taboada GL, Doallo R, Posada D. 2012. jModelTest 2: more models, new heuristics and parallel computing. *Nat Methods.* 9:772
- Iwasaki W, Fukunaga T, Isagozawa R, Yamada K, Maeda Y, Satoh TP, Sado T, Mabuchi K, Takeshima H, Miya M, et al. 2013. Mitofish and mitoannotator: a mitochondrial genome database of fish with an accurate and automatic annotation pipeline. *Mol Biol Evol.* 30:2531–2540.
- Katoh K, Standley DM. 2013. MAFFT multiple sequence alignment software version 7: improvements in performance and usability. *Mol Biol Evol.* 30:772–780.
- Kearse M, Moir R, Wilson A, Stones-Havas S, Cheung M, Sturrock S, Buxton S, Cooper A, Markowitz S, Duran C, et al. 2012. Geneious Basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. *Bioinformatics.* 28:1647–1649.
- Maduna SN, Rossouw C, da Silva C, Soekoe M, Bester-van der Merwe AE. 2017. Species identification and comparative population genetics of four coastal houndsharks based on novel NGS-mined microsatellites. *Ecol Evol.* 7:1462–1425.
- Miller MA, Pfeiffer W, Schwartz T. 2010. Creating the CIPRES Science Gateway for inference of large phylogenetic trees. In *Proceedings of the Gateway Computation and Environment Workshop (GCE)*. Nov 14; New Orleans, LA. p. 1–8.
- Ronquist F, Teslenko M, Van Der Mark P, Ayres DL, Darling A, Höhna S, Larget B, Liu L, Suchard MA, Huelsenbeck JP. 2012. MrBayes 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. *Syst Biol.* 61:539–542.
- Saidi B, Bradai MN, Bouaïn A. 2008. Reproductive biology of the smooth-hound shark *Mustelus mustelus* (L.) in the Gulf of Gabès (south-central Mediterranean Sea). *J Fish Biol.* 72:1343–1354.
- Sambrook J, Russell DW. 2001. *Molecular cloning: a laboratory manual*. New York (NY): Cold Spring Harbor Laboratory Press.
- Smale MJ, Compagno LJV. 1997. Life history and diet of two southern African smoothhound sharks, *Mustelus mustelus* (Linnaeus, 1758) and *Mustelus palumbes* Smith, 1957 (Pisces: Triakidae). *South Afr J Mar Sci.* 18:229–248.
- Teshima K, Koga S. 1973. Studies on sharks. V. Taxonomic characteristics of reproductive organs in Japanese *Mustelus*. *Mar Biol.* 23:337–341.
- Weigmann S. 2016. Annotated checklist of the living sharks, batoids and chimaeras (Chondrichthyes) of the world, with a focus on biogeographical diversity. *J Fish Biol.* 88:837–1037.